

## AMENDMENT TO THE CLAIMS

### WHAT IS CLAIMED IS:

1-11. (canceled)

12. (currently amended) A method of diagnosing breast cancer using a proteome image mining tool, comprising the steps of:

transforming inputted serum proteomes from normal individuals and individuals having breast cancer into two-dimensional images, extracting feature data from the images, generating a proteome standard by computing optimal features from the feature data, and constructing a database consisting of the proteome standard (Step 1);

inputting a serum proteome from a subject of interest, transforming the serum proteome into a two-dimensional image and extracting feature data from the image (Step 2); and

comparing the structure of the serum proteome pattern of the subject with the proteome standard and determining whether the serum proteome of the subject is normal or indicative of said subject having breast cancer (Step 3), wherein the proteome standard is one or more proteins selected from the group consisting of the spots listed in Table 1, wherein said proteome standard comprises molecular weights and isoelectric points of said proteins; and diagnosing said subject with breast cancer when said proteome is indicative of said subject having breast cancer;

wherein said step of producing a proteome standard comprise: a pre-processing step including an image processing step of performing noise filtering, image enhancement, ortho-projection and edge detection from the two-dimensional proteome images, and a feature extraction step of extracting basic features in spot form the image-processed two-dimensional images and producing feature data by labeling each of the extracted features; and

an evolutionary classification step of performing a genetic algorithm to discriminate optimal features playing a critical role in classification among the feature data extracted at the pre-processing step, and extracting optimal feature data and estimation functions by estimating fidelity of the optimal feature data discriminated by the genetic algorithm by a support vector machine using estimation functions and classification error rates;

a fuzzy data mapping step of computing correlations between spots from the two-dimensional images of serum proteomes obtained at the pre-processing step, and classifying the computed features by a statistical method, and quantifying statistical inaccuracy using a fuzzy technique; and

a rule-based classification step of arranging and normalizing the results obtained at the data mapping step, and thus generating a final rule base.

13-14. (canceled)

15. (previously presented) The method of claim 12, wherein the Step 1 further includes the steps of extracting correlations between spots contained in the serum proteome from the two-dimensional images of the serum proteome employing experimental knowledge and a statistical method, and classifying the extracted correlations by a statistical method.

16. (canceled)

17. (previously presented) The method of claim 12, wherein the Step 3 of identifying the existence of breast cancer includes:

a pattern matching step of classifying the serum proteome of the subject into normal or having breast cancer by applying features and estimation functions, extracted upon producing the proteome standard, to the serum proteome of the subject; and

a fine classification step of deducing fine information including correlations between spots, contained in the two-dimensional proteome images.

18. (previously presented) The method of claim 12, further comprising a step of constructing a database consisting of the serum proteome of the subject and analysis results thereof, wherein said step is performed after the Step 3.

19-22. (canceled)